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## SEARCH REQUEST FORM

MAR 21 2005

Access DB#

148326

Scientific and Technical Information Center

(STIC)

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 3-21-05  
 Art Unit: 1635 Phone Number: 202-0765 Serial Number: 09/754,468  
 Mail Box and Bldg/Room Location: 2D28 Results Format Preferred (circle): PAPER DISK E-MAIL  
62018

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: AS Antitumor cell - compo.

Inventors (please provide full names): PATRICK IVERSEN

Earliest Priority Filing Date: 1/4/01

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 47 (20 NA)

— Size limit of 100 NT's.

— No size limits

Please search interference +

regular deter base.

Phenol.

SD

## STAFF USE ONLY

Type of Search		Vendors and cost where applicable
Searcher: <u>Arnold</u>	NA Sequence (#) <u>2</u>	STN _____
Searcher Phone #: <u>2252</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>3/25/05</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>3/28/05</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 07:42:52 ; Search time 3840 Seconds  
(without alignments)  
212.620 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaattctc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 39707814

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Title: US-09-754-468-47

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 675282

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 4	14.8	74.0	94	9 CG629998	CG629998 OST344683
C 5	14.2	71.0	49	9 BX288153	BX288153 Arabidops
C 6	14.2	71.0	84	2 AW466292	AW466292 SWANAC21
C 7	14.2	71.0	85	9 CG505735	CG505735 OST54845
C 8	14.2	71.0	98	9 CL529492	CL529492 HIV40D02
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C 10	14.2	71.0	100	5 BQ856685	BQ856685 QGB5H24.Y
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C 13	13.8	69.0	44	8 AZ834300	AZ834300 2M0116019
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C 17	13.8	69.0	57	4 BI322307	BI322307 Kx19c11.Y
C 18	13.8	69.0	62	1 AI506296	AI506296 VP42a07.x
C 19	13.8	69.0	63	6 CB005039	CB005039 VPC007D11
C 20	13.8	69.0	64	1 AA989601	AA989601 am70b01.s
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31	13.8	69.0	79	2 BP942148	BP942148 nae87f03.
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 88)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-rc@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:59:41 ; Search time 3927 Seconds  
(without alignments)  
207.910 Million cell updates/sec

US-09-754-468-47

Title:

Perfect score: 20

Sequence: 1 gattagcataataaatctc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

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Listing first 45 summaries

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40: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq.\*  
41: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq.\*  
42: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq.\*  
43: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq.\*

44: /cgn2\_6/ptodata/1/pna/US099F\_COMB.seq.\*  
45: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq.\*  
46: /cgn2\_6/ptodata/1/pna/US100B\_COMB.seq.\*  
47: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq.\*  
48: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq.\*  
49: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq.\*  
50: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq.\*  
51: /cgn2\_6/ptodata/1/pna/US103A\_COMB.seq.\*  
52: /cgn2\_6/ptodata/1/pna/US103B\_COMB.seq.\*  
53: /cgn2\_6/ptodata/1/pna/US104A\_COMB.seq.\*  
54: /cgn2\_6/ptodata/1/pna/US104B\_COMB.seq.\*  
55: /cgn2\_6/ptodata/1/pna/US105A\_COMB.seq.\*  
56: /cgn2\_6/ptodata/1/pna/US105B\_COMB.seq.\*  
57: /cgn2\_6/ptodata/1/pna/US106A\_COMB.seq.\*  
58: /cgn2\_6/ptodata/1/pna/US107A\_COMB.seq.\*  
59: /cgn2\_6/ptodata/1/pna/US107B\_COMB.seq.\*  
60: /cgn2\_6/ptodata/1/pna/US107C\_COMB.seq.\*  
61: /cgn2\_6/ptodata/1/pna/US107D\_COMB.seq.\*  
62: /cgn2\_6/ptodata/1/pna/US108A\_COMB.seq.\*  
63: /cgn2\_6/ptodata/1/pna/US108B\_COMB.seq.\*  
64: /cgn2\_6/ptodata/1/pna/US109A\_COMB.seq.\*  
65: /cgn2\_6/ptodata/1/pna/US109B\_COMB.seq.\*  
66: /cgn2\_6/ptodata/1/pna/US109C\_COMB.seq.\*  
67: /cgn2\_6/ptodata/1/pna/US110\_COMB.seq.\*  
68: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq.\*  
69: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq.\*  
70: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq.\*  
71: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq.\*  
72: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq.\*  
73: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq.\*  
74: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq.\*  
75: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*  
76: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq.\*  
77: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq.\*  
78: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq.\*  
79: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq.\*  
80: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*  
81: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq.\*  
82: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq.\*  
83: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq.\*  
84: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq.\*  
85: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq.\*  
86: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq.\*  
87: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq.\*  
88: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq.\*  
89: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*  
90: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*  
91: /cgn2\_6/ptodata/1/pna/US6023A\_COMB.seq.\*  
92: /cgn2\_6/ptodata/1/pna/US6023B\_COMB.seq.\*  
93: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*  
94: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*  
95: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*  
96: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*  
97: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*  
98: /cgn2\_6/ptodata/1/pna/US6029\_COMB.seq.\*  
99: /cgn2\_6/ptodata/1/pna/US6030\_COMB.seq.\*  
100: /cgn2\_6/ptodata/1/pna/US6031\_COMB.seq.\*  
101: /cgn2\_6/ptodata/1/pna/US6032\_COMB.seq.\*  
102: /cgn2\_6/ptodata/1/pna/US6033\_COMB.seq.\*  
103: /cgn2\_6/ptodata/1/pna/US6034\_COMB.seq.\*  
104: /cgn2\_6/ptodata/1/pna/US6035\_COMB.seq.\*  
105: /cgn2\_6/ptodata/1/pna/US6036\_COMB.seq.\*  
106: /cgn2\_6/ptodata/1/pna/US6037\_COMB.seq.\*  
107: /cgn2\_6/ptodata/1/pna/US6038\_COMB.seq.\*  
108: /cgn2\_6/ptodata/1/pna/US6039\_COMB.seq.\*  
109: /cgn2\_6/ptodata/1/pna/US6040\_COMB.seq.\*  
110: /cgn2\_6/ptodata/1/pna/US6041\_COMB.seq.\*  
111: /cgn2\_6/ptodata/1/pna/US6042\_COMB.seq.\*  
112: /cgn2\_6/ptodata/1/pna/US6043\_COMB.seq.\*  
113: /cgn2\_6/ptodata/1/pna/US6044\_COMB.seq.\*  
114: /cgn2\_6/ptodata/1/pna/US6045\_COMB.seq.\*  
115: /cgn2\_6/ptodata/1/pna/US6046\_COMB.seq.\*  
116: /cgn2\_6/ptodata/1/pna/US6047\_COMB.seq.\*

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:52:49 ; Search time 3094 Seconds  
(without alignments)  
246.052 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 05:11:41 ; Search time 400 Seconds  
(without alignments)  
58.914 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5793115 seqs, 589143167 residues

Total number of hits satisfying chosen parameters: 11586230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US12\_NEW\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US13\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:38:33 ; Search time 1670 Seconds  
(without alignments)  
580.302 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:03:09 ; Search time 433 Seconds  
(without alignments)  
273.429 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 06:21:46 ; Search time 1662 Seconds  
(without alignments)  
583.095 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 2238514  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
-----					

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 07:34:21 ; Search time 127 Seconds  
(without alignments)  
257.681 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1330268

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 06:19:36 ; Search time 422 Seconds  
(without alignments)  
280.556 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaatctc 20~

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4530610

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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Mon Mar 28 08:23:20 2005

us-09-754-468-47.sizelim.rnpn

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 07:50:07 ; Search time 396 Seconds  
(without alignments)  
59.509 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5793115 seqs, 589143167 residues

Total number of hits satisfying chosen parameters: 10729062

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 05:27:46 ; Search time 499 Seconds  
(without alignments)  
238.851 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:55:19 ; Search time 129 Seconds  
(without alignments)  
253.686 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaaatctc 20  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 08:17:57 ; Search time 489 Seconds  
(without alignments)  
243.735 Million cell updates/sec

Title: US-09-754-468-47  
Perfect score: 20  
Sequence: 1 gattagcataataaatctc 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 5451806

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES